

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/467,605

DATE: 12/18/96

TIME: 11:47:04

INPUT SET: S14460.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Pietropaolo, Massimo and Eisenbarth, George S.
6
7 (ii) TITLE OF INVENTION: Antigen Associated with Type I Diabetes Mellitus
8
9 (iii) NUMBER OF SEQUENCES: 2
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: LAHIVE & COCKFIELD
13 (B) STREET: 60 State Street, suite 510
14 (C) CITY: Boston
15 (D) STATE: Massachusetts
16 (E) COUNTRY: USA
17 (F) ZIP: 02109-1875
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Floppy disk
21 (B) COMPUTER: IBM PC compatible
22 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER: 08/467,605
27 (B) FILING DATE: 06 June 1995
28 (C) CLASSIFICATION:
29
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: 07/788,118
32 (B) FILING DATE: 01 November 1991
33
34 (viii) ATTORNEY/AGENT INFORMATION:
35 (A) NAME: Silveri, Jean M.
36 (B) REGISTRATION NUMBER: 39,030
37 (C) REFERENCE/DOCKET NUMBER: IMI-001CPDV
38
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: (617)227-7400
41 (B) TELEFAX: (617)227-5941
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

18E 0813
Scheiner

| | | |
|----|---|-----|
| 47 | (A) LENGTH: 1785 base pairs | |
| 48 | (B) TYPE: nucleic acid | |
| 49 | (C) STRANDEDNESS: single | |
| 50 | (D) TOPOLOGY: linear | |
| 51 | | |
| 52 | (ii) MOLECULE TYPE: cDNA | |
| 53 | | |
| 54 | | |
| 55 | (ix) FEATURE: | |
| 56 | (A) NAME/KEY: CDS | |
| 57 | (B) LOCATION: 179..1628 | |
| 58 | | |
| 59 | | |
| 60 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1: | |
| 61 | | |
| 62 | CGGGCGGGGG ATACCCAGG AGATGGGGGT CGAGGAGAGA CCCCGGGGAG TAGAGAGAGA | 60 |
| 63 | | |
| 64 | GAAACTCACT CCCCGAGTCC CCGACCCTCC CCAAGCAAGG TTATAATATA ACTTATCCTC | 120 |
| 65 | | |
| 66 | TCATGCTTTT TTCCTGCCCC TTCTCCCCAA ATCATCAACA ATAGAAGAAG AAGAAAAAC | 178 |
| 67 | | |
| 68 | ATG TCA GGA CAC AAA TGC AGT TAT CCC TGG GAC TTA CAG GAT CGA TAT | 226 |
| 69 | Met Ser Gly His Lys Cys Ser Tyr Pro Trp Asp Leu Gln Asp Arg Tyr | |
| 70 | 1 5 10 15 | |
| 71 | | |
| 72 | GCT CAA GAT AAG TCA GTT GTA AAT AAG ATG CAA CAG AGA TAT TGG GAG | 274 |
| 73 | Ala Gln Asp Lys Ser Val Val Asn Lys Met Gln Gln Arg Tyr Trp Glu | |
| 74 | 20 25 30 | |
| 75 | | |
| 76 | ACG AAG CAG GCC TTT ATT AAA GCC ACA GGG AAG AAG GAA GAT GAA CAT | 322 |
| 77 | Thr Lys Gln Ala Phe Ile Lys Ala Thr Gly Lys Lys Glu Asp Glu His | |
| 78 | 35 40 45 | |
| 79 | | |
| 80 | GTT GTT GCC TCT GAC GCG GAC CTG GAT GCC AAG CTA GAG CTG TTT CAT | 370 |
| 81 | Val Val Ala Ser Asp Ala Asp Leu Asp Ala Lys Leu Glu Leu Phe His | |
| 82 | 50 55 60 | |
| 83 | | |
| 84 | TCA ATT CAG AGA ACC TGT CTG GAC TTA TCG AAA GCA ATT GTA CTC TAT | 418 |
| 85 | Ser Ile Gln Arg Thr Cys Leu Asp Leu Ser Lys Ala Ile Val Leu Tyr | |
| 86 | 65 70 75 80 | |
| 87 | | |
| 88 | CAA CAG AGG ATA TGT TTC TTG TCT CAA GAA GAA AAC GAA CTG GGA AAA | 466 |
| 89 | Gln Gln Arg Ile Cys Phe Leu Ser Gln Glu Glu Asn Glu Leu Gly Lys | |
| 90 | 85 90 95 | |
| 91 | | |
| 92 | TTT CTT CGA TCC CAA GGT TTC CAA GAT AAA ACC AGA GCA GGA AAG ATG | 514 |
| 93 | Phe Leu Arg Ser Gln Gly Phe Gln Asp Lys Thr Arg Ala Gly Lys Met | |
| 94 | 100 105 110 | |
| 95 | | |
| 96 | ATG CAA GCG ACA GGA AAG GCC CTC TGC TTT TCT TCC CAG CAA AGG TTG | 562 |
| 97 | Met Gln Ala Thr Gly Lys Ala Leu Cys Phe Ser Ser Gln Gln Arg Leu | |
| 98 | 115 120 125 | |
| 99 | | |

RAW SEQUENCE LISTING PATENT APPLICATION US/08/467,605

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TIME: 11:47:11

INPUT SET: S14460.raw

| | | |
|-----|---|------|
| 100 | GCC TTA CGA AAT CCT TTG TGT CGA TTT CAC CAA GAA GTG GAG ACT TTT | 610 |
| 101 | Ala Leu Arg Asn Pro Leu Cys Arg Phe His Gln Glu Val Glu Thr Phe | |
| 102 | 130 135 140 | |
| 103 | | |
| 104 | CGG CAT CGG GCC ATC TCA GAT ACT TGG CTG ACG GTG AAC CGC ATG GAA | 658 |
| 105 | Arg His Arg Ala Ile Ser Asp Thr Trp Leu Thr Val Asn Arg Met Glu | |
| 106 | 145 150 155 160 | |
| 107 | | |
| 108 | CAG TGC AGG ACG GAA TAT AGA GGA GCA CTA TTA TGG ATG AAG GAC GTG | 706 |
| 109 | Gln Cys Arg Thr Glu Tyr Arg Gly Ala Leu Leu Trp Met Lys Asp Val | |
| 110 | 165 170 175 | |
| 111 | | |
| 112 | TCT CAG GAG CTT GAT CCA GAC CTC TAC AAG CAA ATG GAG AAG TTC AGG | 754 |
| 113 | Ser Gln Glu Leu Asp Pro Asp Leu Tyr Lys Gln Met Glu Lys Phe Arg | |
| 114 | 180 185 190 | |
| 115 | | |
| 116 | AAG GTG CAA ACA CAA GTG CGC CTT GCA AAA AAA AAC TTT GAC AAA TTG | 802 |
| 117 | Lys Val Gln Thr Gln Val Arg Leu Ala Lys Lys Asn Phe Asp Lys Leu | |
| 118 | 195 200 205 | |
| 119 | | |
| 120 | AAG ATG GAT GTG TGT CAA AAA GTG GAT CTT CTT GGA GCG AGC AGA TGC | 850 |
| 121 | Lys Met Asp Val Cys Gln Lys Val Asp Leu Leu Gly Ala Ser Arg Cys | |
| 122 | 210 215 220 | |
| 123 | | |
| 124 | AAT CTC TTG TCT CAC ATG CTA GCA ACA TAC CAG ACC ACT CTG CTT CAT | 898 |
| 125 | Asn Leu Leu Ser His Met Leu Ala Thr Tyr Gln Thr Thr Leu Leu His | |
| 126 | 225 230 235 240 | |
| 127 | | |
| 128 | TTT TGG GAG AAA ACT TCT CAC ACT ATG GCA GCC ATC CAT GAG AGT TTC | 946 |
| 129 | Phe Trp Glu Lys Thr Ser His Thr Met Ala Ala Ile His Glu Ser Phe | |
| 130 | 245 250 255 | |
| 131 | | |
| 132 | AAA GGT TAT CAA CCA TAT GAA TTT ACT ACT TTA AAG AGC TTA CAA GAC | 994 |
| 133 | Lys Gly Tyr Gln Pro Tyr Glu Phe Thr Thr Leu Lys Ser Leu Gln Asp | |
| 134 | 260 265 270 | |
| 135 | | |
| 136 | CCT ATG AAA AAA TTA GTT GAG AAA GAA GAG AAG AAG AAA ATC AAC CAG | 1042 |
| 137 | Pro Met Lys Lys Leu Val Glu Lys Glu Glu Lys Lys Lys Ile Asn Gln | |
| 138 | 275 280 285 | |
| 139 | | |
| 140 | CAG GAA AGT ACA GAT GCA GCC GTG CAG CAG CCG AGC CAA TTA ATT TCA | 1090 |
| 141 | Gln Glu Ser Thr Asp Ala Ala Val Gln Gln Pro Ser Gln Leu Ile Ser | |
| 142 | 290 295 300 | |
| 143 | | |
| 144 | TTA GAG GAA GAA AAC CAG CGC AAG GAA TCC TCT AGT TTT AAG ACT GAA | 1138 |
| 145 | Leu Glu Glu Glu Asn Gln Arg Lys Glu Ser Ser Ser Phe Lys Thr Glu | |
| 146 | 305 310 315 320 | |
| 147 | | |
| 148 | GAT GGA AAA AGT ATT TTA TCT GCC TTA GAC AAA GGC TCT ACA CAT ACT | 1186 |
| 149 | Asp Gly Lys Ser Ile Leu Ser Ala Leu Asp Lys Gly Ser Thr His Thr | |
| 150 | 325 330 335 | |
| 151 | | |
| 152 | GCA TGC TCA GGA CCC ATA GAT GAA CTA TTA GAC ATG AAA TCT GAG GAA | 1234 |

RAW SEQUENCE LISTING PATENT APPLICATION US/08/467,605

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153  Ala Cys Ser Gly Pro Ile Asp Glu Leu Leu Asp Met Lys Ser Glu Glu
154              340              345              350
155
156  GGT GCT TGC CTG GGA CCA GTG GCA GGG ACC CCG GAA CCT GAA GGT GCT      1282
157  Gly Ala Cys Leu Gly Pro Val Ala Gly Thr Pro Glu Pro Glu Gly Ala
158              355              360              365
159
160  GAC AAA GAT GAC CTG CTG CTG TTG AGT GAG ATC TTC AAT GCT TCC TCC      1330
161  Asp Lys Asp Asp Leu Leu Leu Leu Ser Glu Ile Phe Asn Ala Ser Ser
162              370              375              380
163
164  TTG GAA GAG GGC GAG TTC AGC AAA GAG TGG GCC GCT GTG TTT GGA GAC      1378
165  Leu Glu Glu Gly Glu Phe Ser Lys Glu Trp Ala Ala Val Phe Gly Asp
166  385              390              395              400
167
168  GGC CAA GTG AAG GAG CCA GTG CCC ACT ATG GCC CTG GGA GAG CCA GAC      1426
169  Gly Gln Val Lys Glu Pro Val Pro Thr Met Ala Leu Gly Glu Pro Asp
170              405              410              415
171
172  CCC AAG GCC CAG ACA GGC TCA GGT TTC CTT CCT TCG CAG CTT TTA GAC      1474
173  Pro Lys Ala Gln Thr Gly Ser Gly Phe Leu Pro Ser Gln Leu Leu Asp
174              420              425              430
175
176  CAA AAT ATG AAA GAC TTA CAG GCC TCG CTA CAA GAA CCT GCT AAG GCT      1522
177  Gln Asn Met Lys Asp Leu Gln Ala Ser Leu Gln Glu Pro Ala Lys Ala
178              435              440              445
179
180  GCC TCA GAC CTG ACT GCC TGG TTC AGC CTC TTC GCT GAC CTC GAC CCA      1570
181  Ala Ser Asp Leu Thr Ala Trp Phe Ser Leu Phe Ala Asp Leu Asp Pro
182              450              455              460
183
184  CTC TCA AAT CCT GAT GCT GTT GGG AAA ACC GAT AAA GAA CAC GAA TTG      1618
185  Leu Ser Asn Pro Asp Ala Val Gly Lys Thr Asp Lys Glu His Glu Leu
186  465              470              475              480
187
188  CTC AAT GCA TGA ATCTGTAC CCTTCGGAGG GCACTCACAT GCCGCCCCCA      1668
189  Leu Asn Ala *
190
191
192  GCAGCTCCCC TGGGGGCTAG CAGAAGTATA AAGTGATCAG TATGCTGTTT TAATAATTAT      1728
193
194  GTGCCATTTT AATAAAATGA AAGGGTCAAC GGCCCTGTTA AAAAAAAAAA AAAAAAAA      1785
195
196
197  (2) INFORMATION FOR SEQ ID NO:2:
198
199      (i) SEQUENCE CHARACTERISTICS:
200          (A) LENGTH: 483 amino acids
201          (B) TYPE: amino acid
202          (D) TOPOLOGY: linear
203
204      (ii) MOLECULE TYPE: protein
205

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INPUT SET: S14460.raw

| | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: | | | | | | | | | | | | | | | | |
|-----|---|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 206 | | | | | | | | | | | | | | | | | |
| 207 | | | | | | | | | | | | | | | | | |
| 208 | Met | Ser | Gly | His | Lys | Cys | Ser | Tyr | Pro | Trp | Asp | Leu | Gln | Asp | Arg | Tyr | |
| 209 | 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| 210 | | | | | | | | | | | | | | | | | |
| 211 | Ala | Gln | Asp | Lys | Ser | Val | Val | Asn | Lys | Met | Gln | Gln | Arg | Tyr | Trp | Glu | |
| 212 | | | | 20 | | | | | 25 | | | | | 30 | | | |
| 213 | | | | | | | | | | | | | | | | | |
| 214 | Thr | Lys | Gln | Ala | Phe | Ile | Lys | Ala | Thr | Gly | Lys | Lys | Glu | Asp | Glu | His | |
| 215 | | | 35 | | | | | 40 | | | | | 45 | | | | |
| 216 | | | | | | | | | | | | | | | | | |
| 217 | Val | Val | Ala | Ser | Asp | Ala | Asp | Leu | Asp | Ala | Lys | Leu | Glu | Leu | Phe | His | |
| 218 | | 50 | | | | | 55 | | | | | 60 | | | | | |
| 219 | | | | | | | | | | | | | | | | | |
| 220 | Ser | Ile | Gln | Arg | Thr | Cys | Leu | Asp | Leu | Ser | Lys | Ala | Ile | Val | Leu | Tyr | |
| 221 | 65 | | | | | 70 | | | | | 75 | | | | | 80 | |
| 222 | | | | | | | | | | | | | | | | | |
| 223 | Gln | Gln | Arg | Ile | Cys | Phe | Leu | Ser | Gln | Glu | Glu | Asn | Glu | Leu | Gly | Lys | |
| 224 | | | | 85 | | | | | | 90 | | | | | 95 | | |
| 225 | | | | | | | | | | | | | | | | | |
| 226 | Phe | Leu | Arg | Ser | Gln | Gly | Phe | Gln | Asp | Lys | Thr | Arg | Ala | Gly | Lys | Met | |
| 227 | | | | 100 | | | | | 105 | | | | | 110 | | | |
| 228 | | | | | | | | | | | | | | | | | |
| 229 | Met | Gln | Ala | Thr | Gly | Lys | Ala | Leu | Cys | Phe | Ser | Ser | Gln | Gln | Arg | Leu | |
| 230 | | | 115 | | | | | 120 | | | | | 125 | | | | |
| 231 | | | | | | | | | | | | | | | | | |
| 232 | Ala | Leu | Arg | Asn | Pro | Leu | Cys | Arg | Phe | His | Gln | Glu | Val | Glu | Thr | Phe | |
| 233 | | 130 | | | | | 135 | | | | | 140 | | | | | |
| 234 | | | | | | | | | | | | | | | | | |
| 235 | Arg | His | Arg | Ala | Ile | Ser | Asp | Thr | Trp | Leu | Thr | Val | Asn | Arg | Met | Glu | |
| 236 | 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| 237 | | | | | | | | | | | | | | | | | |
| 238 | Gln | Cys | Arg | Thr | Glu | Tyr | Arg | Gly | Ala | Leu | Leu | Trp | Met | Lys | Asp | Val | |
| 239 | | | | | 165 | | | | | 170 | | | | | 175 | | |
| 240 | | | | | | | | | | | | | | | | | |
| 241 | Ser | Gln | Glu | Leu | Asp | Pro | Asp | Leu | Tyr | Lys | Gln | Met | Glu | Lys | Phe | Arg | |
| 242 | | | | 180 | | | | | 185 | | | | | 190 | | | |
| 243 | | | | | | | | | | | | | | | | | |
| 244 | Lys | Val | Gln | Thr | Gln | Val | Arg | Leu | Ala | Lys | Lys | Asn | Phe | Asp | Lys | Leu | |
| 245 | | | 195 | | | | | 200 | | | | | 205 | | | | |
| 246 | | | | | | | | | | | | | | | | | |
| 247 | Lys | Met | Asp | Val | Cys | Gln | Lys | Val | Asp | | | | | | | | |